Amendments to the Drawings:

The attached two sheets of drawings include changes to Figs. 5 and 6, and replace the original sheets including Figs. 5 and 6. Figs. 5 and 6 have been amended to delete the text labels "Table 1" and "Table 2," respectively.

Attachment: Replacement Sheet
Annotated Sheet Showing Changes

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REMARKS

INTRODUCTION

This Amendment is in response to the Office Action dated December 27, 2005. Applicants sincerely thank Examiner Zhou for the courtesies extended to Applicants' representative, Scott Balderston, during the personal interview conducted June 15, 2006. Applicants have amended the application in light of the Office Action to address all objections to the specification and drawings, and all rejections of the claims. Favorable reconsideration is respectfully requested.

OBJECTIONS TO THE SPECIFICATION AND DRAWINGS

The Office Action objected to the title of the invention. Applicants have amended the title in response to that objection. The Office Action objected to the reference to "AB1" format for certain computer data noted, for instance, at pages 21 and 30 of the specification. Applicants respectfully submit that the file extension or file identifier "AB1" is in fact a type of file format or identifier known in the art. Applicants have submitted an Information Disclosure Statement on June 27, 2006, submitting an excerpt from a document entitled "ABI Prism® 3000 Genetic Analyzer" making a notation of that file format at page 5-9.

The Office Action objected to the Internet hyperlink "www.phrap.org" referenced at page 3, line 14, of the specification. Applicants have truncated the reference to "phrap.org" so that reference does not represent a full embedded hyperlink. The Office Action objected to the drawings and specification because the data shown in Figs. 5 and 6 were labeled as "Table 1" and "Table 2"

respectively, but shown as figures in the drawings. Applicants have deleted the labels "Table 1" and "Table 2" in Figs. 5 and 6 and conformed the specification to refer to Figs. 5 and 6, accordingly.

Applicants have therefore considered and duly responded to all of the objections to the specification and drawings, which are therefore overcome. Reconsideration and withdrawal of the objections are respectfully requested.

REJECTIONS OF CLAIMS UNDER 35 U.S.C. §112, SECOND PARAGRAPH

The Office Action rejected claims 1-18 and 43 under 35 U.S.C. §112, second paragraph for indefiniteness due to the term "reportable ranges" in claims 1 and 43. Applicants have amended claims 1 and 43 to recite "wherein the reportable ranges comprise base sequence ranges related to the at least one sample, usable for comparison matching". As discussed in the specification, for instance, at page 19, lines 10-22 and at page 26, line 11 – page 27, line 2, those "reportable ranges" can, in various embodiments and generally speaking, represent DNA, mtDNA, or other base sequence ranges that have been determined to be sufficiently unambiguous or reliable to use for comparison matching purposes. Claims 1-18 and 43 are therefore adequately clear, and it is respectfully submitted that the rejection is therefore overcome.

Applicants understand the Office Action to have rejected all dependent claims which recite the term "major and minor bases," under 35 U.S.C. §112, second paragraph, as being indefinite. Claims 2 and 4-12 recite that term. Applicants respectfully submit that the term "major and minor bases" would have been adequately clear to a person skilled in the art at the time the application was filed, so that this rejection is overcome. Applicants submit that "major and minor

bases" would be understood by persons skilled in the art to refer to bases that are associated with major peaks and minor peaks of an electropherogram generated by base-calling or sequencing operations. Applicants have submitted an Information Disclosure Statement on June 27, 2006, submitting a document entitled "Comparison of PowerPlex™ 16, Plower Plex™ 1.1/2.1, and ABI Ampf/STR™ Profiler PlusTM/COfiler™ for Forensic Use". That document refers, for example, at page 42:241, to the association of alleles with major and minor peaks in electropherograms generated by ABI Prism™ hardware, consistent with this connotation. Various peaks generated by such operations are, for example, illustrated in Applicants' Fig. 1, and described, for instance, in the specification at page 16, lines 16-22. Applicants respectfully submit that the term "major and minor bases" is adequately clear, and that the rejection is overcome.

The Office Action rejected claim 18 under 35 U.S.C. §112, second paragraph, as being indefinite due to the language "wherein the sequence information corresponds to mitochondrial sequence information." Applicants have amended this language to recite that the sequence information "comprises mitochondrial sequence information." All rejections of claims 1-18 and 43, under 35 U.S.C. §112, second paragraph, are thereby duly addressed and overcome. Reconsideration and withdrawal of the rejection are respectfully requested.

CONCLUSION

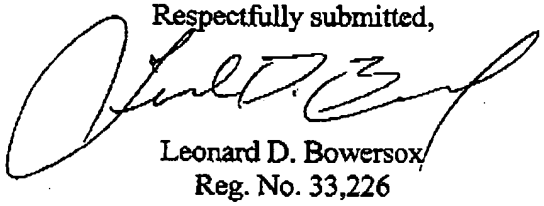
In view of the foregoing remarks, Applicants respectfully request favorable reconsideration of the present application and a timely allowance of the pending claims.

Application No. 10/672,937
Response to Notice and Corrected Amendment dated October 11, 2006
In Response to Notice of Non-Compliant Amendment Dated September 12, 2006

Should the Examiner deem that any further action by Applicants or Applicants' undersigned representative is desirable and/or necessary, the Examiner is invited to telephone the undersigned at the number set forth below.

If there are any other fees due in connection with the filing of this response, please charge the fees to deposit Account No. 50-0925. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such extension is requested and should also be charged to said Deposit Account.

Respectfully submitted,



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Enclosures: Corrected Figs. 5 and 6
Annotated Version Showing Corrections to Figs. 5 and 6

System components and tunable parameters

Program	Function performed
BlastParse.pl	Parse BLAST output
mark_substitution_heteroplasmy.pl	Mark ambiguous base calls
extract_SE_consensus.pl	Extract a consensus sequence from a phrap polyphred run, replacing low quality bases with '?', and polyphred rank 1 bases with 'N'.
compute_coverage.pl	Calculates overall, forward strand, and reverse strand coverage for all bases in the consensus sequence
count_hv1_deletes.pl	Count deletions in HV1 relative to the rCRS
border_index.pl	Compute start and end positions of HV1 and HV2 regions.
fix_mitotype_reporting_range.pl	Output a mtDNA profile based on input variants list and reportable range.
find_bad_traces_from_blast_report.pl	Reject reads that do not align appropriately to the rCRS
determineReadTypes.pl	Adds template name, template type, and primer type to phred output files.
seq2delta_vs	Align mtDNA profile to rCRS and report variants according to nomenclature.
calculate_coverage_mitotype.pl	Mask mtDNA consensus sequence based on required coverage and calculated coverage
count_hv1_inserts.pl	Count insertions in HV1 relative to the rCRS
generate_hv_mask_fasta_files.pl	Extract the HV1 portion and HV2 portion of the mtDNA consensus sequence, based on the computed HV1 and HV2 regions.
flip_fasta.pl	Invert an X masked sequence output by cross_match

FIG. 5

	Assessment 1	Assessment 2
Total True Positives: $N_{automated} = N_{manual}$	16	10
Total True Negatives: $A_{automated} = A_{manual}$	77,358	110,354
Total False Positives: $N_{automated} = A_{manual}$	95	807
Total False Negatives: $A_{automated} = N_{manual}$	6[a]	14
Total Incorrect	0	0
Sensitivity: TP/(TP+FN)	72.73%	41.67%
Specificity: TN/(TN+FP)	99.88%	99.27%
Positive Predictive Value: TP/(TP+FP)	14.41%	1.22%
Negative Predictive Value: TN/(TN+FN)	99.99%	99.99%

[a]Predominate base correctly called
Differences take into account the consensus of the two analysts

FIG. 6

ANNOTATED SHEET

Table 1

System components and tunable parameters

Program	Function performed
BlastParse.pl	Parse BLAST output
mark_substitution_heteroplasmy.pl	Mark ambiguous base calls
extract_SE_consensus.pl	Extract a consensus sequence from a phrap polyphred run, replacing low quality bases with '?', and polyphred rank 1 bases with 'N'.
compute_coverage.pl	Calculates overall, forward strand, and reverse strand coverage for all bases in the consensus sequence
count_hv1_deletes.pl	Count deletions in HV1 relative to the rCRS
border_index.pl	Compute start and end positions of HV1 and HV2 regions.
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find_bad_traces_from_blast_report.pl	Reject reads that do not align appropriately to the rCRS
determineReadTypes.pl	Adds template name, template type, and primer type to phred output files.
seq2delta_vs	Align mtDNA profile to rCRS and report variants according to nomenclature.
calculate_coverage_mitotype.pl	Mask mtDNA consensus sequence based on required coverage and calculated coverage
count_hv1_inserts.pl	Count insertions in HV1 relative to the rCRS
generate_hv_mask_fasta_files.pl	Extract the HV1 portion and HV2 portion of the mtDNA consensus sequence, based on the computed HV1 and HV2 regions.
flip_fasta.pl	Invert an X masked sequence output by cross_match

FIG. 5

ANNOTATED SHEET

Table 2

	Assessment 1	Assessment 2
Total True Positives: $N_{automated} = N_{manual}$	16	10
Total True Negatives: $A_{automated} = A_{manual}$	77,358	110,354
Total False Positives: $N_{automated} = A_{manual}$	95	807
Total False Negatives: $A_{automated} = N_{manual}$	6[a]	14
Total Incorrect	0	0
Sensitivity: TP/(TP+FN)	72.73%	41.67%
Specificity: TN/(TN+FP)	99.88%	99.27%
Positive Predictive Value: TP/(TP+FP)	14.41%	1.22%
Negative Predictive Value: TN/(TN+FN)	99.99%	99.99%

[a]Predominate base correctly called
Differences take into account the consensus of the two analysts

FIG. 6